SEQUENCE LISTING

<110> LADNER, ROBERT C.

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<130> DYAX/004

<140> 10/026,925
<141> 2001-12-18

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<170> PatentIn Ver. 2.1

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<220>
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Gly

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<220>
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1 5 10 15

Gly

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CDR3 vector

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CDR3 vector

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Gly

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Tyr Trp Gly

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Phe Asp Tyr Trp Gly
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CDR3 vector

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Xaa Xaa Tyr Phe Asp Tyr Trp Gly
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Xaa Xaa Xaa Tyr Phe Asp Tyr Trp Gly
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Tyr Xaa Xaa Xaa Tyr Phe Asp Tyr Trp Gly
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Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Thr
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<220>
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<220>
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<400> 17
Gln Gln Xaa Xaa Xaa Xaa Pro Pro Xaa Thr
1 5 10

<210> 18
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<220>
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<223> Any amino acid except Cys

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<400> 19
Xaa Ser Tyr Xaa Xaa Ser Xaa Xaa Xaa Val
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Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Ser Ser
1 5 10

<210> 21
<211> 15
<212> PRT
<213> Homo sapiens

<400> 21
Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10 15

<210> 22
<211> 5
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Tyr Tyr Cys Ala Arg
1 5

<210> 23
<211> 323
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vector with CDR1/2 diversity

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<222> (111)..(113)
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  1               5                  10                  15

cct ggt ggt tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc    95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
             20                  25                  30

tct nnn tac nnn atg nnn tgg gtt cgc caa gct cct ggt aaa ggt ttg    143
Ser Xaa Tyr Xaa Met Xaa Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
         35                  40                  45
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gag tgg gtt tct nnn atc nnn nnn tct ggt ggc nnn act nnn tat gct   191
Glu Trp Val Ser Xaa Ile Xaa Xaa Ser Gly Gly Xaa Thr Xaa Tyr Ala
     50                  55                  60

gac tcc gtt aaa ggt cgc ttc act atc tct aga gac aac tct aag aat   239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65                  70                  75                  80

act ctc tac ttg cag atg aac agc tta agg gct gag gac acc gct gtc   287
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                 85                  90                  95

tac tac tgc gcc aaa gac tat gaa ggt act ggt tat                   323
Tyr Tyr Cys Ala Lys Asp Tyr Glu Gly Thr Gly Tyr
            100                 105
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1 5 10 15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

Ser Xaa Tyr Xaa Met Xaa Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ser Xaa Ile Xaa Xaa Ser Gly Gly Xaa Thr Xaa Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Lys Asp Tyr Glu Gly Thr Gly Tyr
100 105

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1 5 10 15

<210> 26
<211> 15
<212> PRT
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Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10 15

<210> 27
<211> 55
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<220>
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<222> (27)..(29)
<223> a, c, t or g

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<223> a, c, t or g

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<210> 28
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<210> 29
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tgggttcgcc aagctcctgg ttgctcactc 30

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<223> a, c, t or g

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<223> a, c, t or g

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gttaaagg 68

<210> 33
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<212> DNA
<213> Artificial Sequence

<220>
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<223> a, c, t or g

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gttaaagg 68

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<223> a, c, t or g

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aaggg 65

<210> 37
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<220>
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oligonucleotide

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<210> 39
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<220>
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<220>
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<210> 43
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<220>
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<400> 43
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<210> 45
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<223> a, c, t or g

<400> 45
ccgctgtcta ctactgcgcc mrnnnnnnnn nnnnnnnnnn ntacttcgat tactggggcc 60
aagg 64

<210> 46
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (23)..(47)
<223> a, c, t or g

<400> 46
ccgctgtcta ctactgcgcc mrnnnnnnnn nnnnnnnnnn nnnnnnntac ttcgattact 60
ggggccaagg 70

<210> 47
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (24)..(32)
<223> a, c, t or g

<220>
<221> modified_base

<222> (38)
<223> a, c, t or g

<220>
<221> modified_base
<222> (45)..(53)
<223> a, c, t or g

<400> 47
ccgctgtcta ctactgcgcc cgtnnnnnnn nntctdsntc ttrbnnnnnn nnntacttcg 60
attactgggg ccaagg 76

<210> 48
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (23)..(32)
<223> a, c, t or g

<220>
<221> modified_base
<222> (42)..(47)
<223> a, c, t or g

<220>
<221> modified_base
<222> (54)..(56)
<223> a, c, t or g

<400> 48
ccgctgtcta ctactgcgcc mrnnnnnnnn nntgctctgg tnnnnnntgc tatnnntact 60
tcgattactg gggccaagg 79

<210> 49
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (23)..(29)
<223> a, c, t or g

<220>
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<222> (33)..(35)
<223> a, c, t or g

<220>
<221> modified_base
<222> (48)..(62)
<223> a, c, t or g

<400> 49
ccgctgtcta ctactgcgcc mrnnnnnnnt ctnnnactat cttcggtnnn nnnnnnnnnn 60
nntacttcga ttactggggc caagg 85

<210> 50
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
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<222> (24)..(32)
<223> a, c, t or g

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<222> (41)
<223> a, c, t or g

<220>
<221> modified_base
<222> (47)
<223> a, c, t or g

<220>
<221> modified_base
<222> (50)
<223> a, c, t or g

<220>
<221> modified_base
<222> (57)..(65)
<223> a, c, t or g

<400> 50
ccgctgtcta ctactgcgcc cgtnnnnnnn nntattacgr ntctdsndsn tactatnnnn 60
nnnnntactt cgattactgg ggccaagg 88

<210> 51
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (24)..(35)
<223> a, c, t or g

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<222> (44)
<223> a, c, t or g

<220>
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<222> (47)
<223> a, c, t or g

<220>
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<222> (50)..(53)
<223> a, c, t or g

<220>
<221> modified_base
<222> (60)..(68)
<223> a, c, t or g

<400> 51
ccgctgtcta ctactgcgcc cgtnnnnnnn nnnnntattg cdsndsnrvn nnntgctatn 60
nnnnnnnnta cttcgattac tggggccaag g 91

<210> 52
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3-23: JH4 vector with stuffers

<220>
<221> CDS
<222> (3)..(107)

<220>
<221> CDS
<222> (114)..(155)

<220>
<221> CDS
<222> (159)..(164)

<220>
<221> CDS
<222> (168)..(227)

<400> 52
cc atg gcc gaa gtt caa ttg tta gag tct ggt ggc ggt ctt gtt cag 47
Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

cct ggt ggt tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc 95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

tct tcg tac gct tagtaa tgg gtt cgc caa gct cct ggt aaa ggt ttg 143
Ser Ser Tyr Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtt tct taa cct agg tag act atc tct aga gac aac tct aag 191
Glu Trp Val Ser Pro Arg Thr Ile Ser Arg Asp Asn Ser Lys
50 55 60

aat act ctc tac ttg cag atg aac agc tta agg gct tagtaaaggc cttaa 242
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
65 70

<210> 53
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3-23: JH4
vector with stuffers

<400> 53
Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30

Ser Ser Tyr Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Ser Pro Arg Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
50 55 60

Leu Gln Met Asn Ser Leu Arg Ala
65 70

<210> 54
<211> 952
<212> DNA
<213> Homo sapiens

<220>
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<222> (206)..(907)

<220>
<221> modified_base
<222> (344)..(346)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (350)..(361)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (413)..(415)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (422)..(424)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (428)..(433)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (536)..(547)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (551)..(553)
<223> a, c, t, g, other or unknown

<400> 54
gaggaccatt gggccccctc cgagactctc gagcgcaacg caattaatgt gagttagctc 60

actcattagg caccccaggc tttacacttt atgcttccgg ctcgtatgtt gtgtggaatt 120

gtgagcggat aacaatttca cacaggaaac agctatgacc atgattacgc caagctttgg 180

agccttttt ttggagattt tcaac gtg aag aag ctc cta ttt gct atc ccg 232
Met Lys Lys Leu Leu Phe Ala Ile Pro
1 5

ctt gtc gtt ccg ttt tac agc cat agt gca caa tcc gtc ctt act caa 280
Leu Val Val Pro Phe Tyr Ser His Ser Ala Gln Ser Val Leu Thr Gln
10 15 20 25

tct cct ggc act ctt tcg cta agc ccg ggt gaa cgt gct acc tta agt 328
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
30 35 40

tgc cgt gct tcc cag nnn gtt nnn nnn nnn nnn ctt gct tgg tat caa 376
Cys Arg Ala Ser Gln Xaa Val Xaa Xaa Xaa Xaa Leu Ala Trp Tyr Gln
45 50 55

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cag aaa cct ggt cag gcg ccg cgt tta ctt att tat nnn gct tct nnn   424
Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Xaa Ala Ser Xaa
        60                  65                  70

cgc nnn nnn ggg atc ccg gac cgt ttc tct ggc tct ggt tca ggt act   472
Arg Xaa Xaa Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
     75                  80                  85

gac ttt acc ctt act att tct aga ttg gaa cct gaa gac ttc gct gtt   520
Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val
 90                  95                 100                 105

tat tat tgc caa cag nnn nnn nnn nnn cct nnn act ttc ggt caa ggt   568
Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Thr Phe Gly Gln Gly
                110                 115                 120

acc aag gtt gaa atc aag cgt acg gtt gcc gct cct agt gtg ttt atc   616
Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
            125                 130                 135

ttt cct cct tct gac gaa caa ttg aag tca ggt act gct tct gtc gta   664
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
        140                 145                 150

tgt ttg ctc aac aat ttc tac cct cgt gaa gct aaa gtt cag tgg aaa   712
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
    155                 160                 165

gtc gat aac gcg ttg cag tcg ggt aac agt caa gaa tcc gtc act gaa   760
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
170                 175                 180                 185

cag gat agt aag gac tct acc tac tct ttg tcc tct act ctt act tta   808
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
                190                 195                 200

tca aag gct gat tat gag aag cat aag gtc tat gct tgc gaa gtt acc   856
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
            205                 210                 215

cac cag ggt ctg agc tcc cct gtt acc aaa agt ttc aac cgt ggt gaa   904
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
        220                 225                 230

tgc taatagggcg cgccacgcat ctctaagcgg ccgcaacagg aggag            952
Cys
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<210> 55
<211> 234
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (47)
<223> Any amino acid

<220>
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<222> (49)..(52)
<223> Any amino acid

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<222> (70)
<223> Any amino acid

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<221> MOD_RES
<222> (73)
<223> Any amino acid

<220>
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<222> (75)..(76)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (111)..(114)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (116)
<223> Any amino acid

<400> 55
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
1 5 10 15

His Ser Ala Gln Ser Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
20 25 30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Xaa Val
35 40 45

Xaa Xaa Xaa Xaa Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Xaa Ala Ser Xaa Arg Xaa Xaa Gly Ile Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Xaa Xaa
100 105 110

Xaa Xaa Pro Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 56
<211> 732
<212> DNA
<213> Homo sapiens

<220>
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<222> (30)..(686)

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<222> (108)..(110)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (117)..(119)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (126)..(137)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (189)..(200)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (306)..(320)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (324)..(335)
<223> a, c, t, g, other or unknown

<400> 56

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gaggaccatt gggcccctta ctccgtgac agt gca caa tcc gct ctc act cag   53
                                Ser Ala Gln Ser Ala Leu Thr Gln
                                  1               5

cct gct agc gtt tcc ggg tca cct ggt caa agt atc act att tct tgt   101
Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys
     10                  15                  20

aca ggt nnn tct tct nnn gtt ggc nnn nnn nnn nnn gtt tct tgg tat   149
Thr Gly Xaa Ser Ser Xaa Val Gly Xaa Xaa Xaa Xaa Val Ser Trp Tyr
 25                  30                  35                  40

caa caa cac ccg ggc aag gcg ccg aag ttg atg atc tac nnn nnn nnn   197
Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Xaa Xaa Xaa
                 45                  50                  55

nnn cgt cct tct ggt gtt agc aat cgt ttc tcc gga tct aaa tcc ggt   245
Xaa Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly
             60                  65                  70

aat acc gca agc tta act atc tct ggt ctg cag gct gaa gac gag gct   293
Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala
         75                  80                  85

gac tac tat tgt nnn nnn nnn nnn nnn tct nnn nnn nnn nnn gtc ttc   341
Asp Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Val Phe
     90                  95                  100

ggc ggt ggt acc aaa ctt act gtc ctc ggt caa cct aag gct gct cct   389
Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
105                 110                 115                 120

tcc gtt act ctc ttc cct cct agt tct gaa gag ctt caa gct aac aag   437
Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
                125                 130                 135

gct act ctt gtt tgc ttg atc agt gac ttt tat cct ggt gct gtt act   485
Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
            140                 145                 150

gtc gct tgg aaa gcc gat tct tct cct gtt aaa gct ggt gtt gag acg   533
Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
        155                 160                 165

acc act cct tct aaa caa tct aac aat aag tac gct gcg agc tct tat   581
Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
    170                 175                 180

ctt tct ctc acc cct gaa caa tgg aag tct cat aaa tcc tat tcc tgt   629
Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
185                 190                 195                 200

caa gtt act cat gaa ggt tct acc gtt gaa aag act gtt gcc cct act   677
Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
                205                 210                 215
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gag tgt tct tagtgaggcg cgccaacgat gttcaaggcg gccgcaacag gaggag 732
Glu Cys Ser

<210> 57
<211> 219
<212> PRT
<213> Homo sapiens

<220>
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<222> (27)
<223> Any amino acid

<220>
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<222> (33)..(36)
<223> Any amino acid

<220>
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<222> (54)..(57)
<223> Any amino acid

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<222> (93)..(97)
<223> Any amino acid

<220>
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<222> (99)..(102)
<223> Any amino acid

<400> 57
Ser Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro
1 5 10 15

Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Xaa Ser Ser Xaa Val Gly
20 25 30

Xaa Xaa Xaa Xaa Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro
35 40 45

Lys Leu Met Ile Tyr Xaa Xaa Xaa Xaa Arg Pro Ser Gly Val Ser Asn
50 55 60

Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser
65 70 75 80

Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Xaa Xaa Xaa Xaa
85 90 95

Xaa Ser Xaa Xaa Xaa Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val
100 105 110

Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
115 120 125

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
130 135 140

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
145 150 155 160

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
165 170 175

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
180 185 190

Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
195 200 205

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 58
gctctggtca acttaagggc tgagg 25

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 59
gctctggtca acttaagggc tgaggacacc gctgtctact actgcgcc 48

<210> 60
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 60
tacttcgatt acttgggcca aggtaccctg gtcacctcgc tccacc 46

<210> 61
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 61
ggtaccctgg tcacctcgct ccacc 25

<210> 62
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 62
ggtctcagtt gctaagcccg ggtgaacgtg ctaccttaag ttgccgtgct tcccag 56

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 63
ggtctcagtt gctaagcccg ggtg 24

<210> 64
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 64
cttgcttggt atcaacagaa acctggtcag gcgccaagtc gtgtc 45

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 65
cctggtcagg cgccaagtcg tgtc 24

<210> 66
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (28)..(30)
<223> a, c, t or g

<220>
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<222> (34)..(42)
<223> a, c, t or g

<400> 66
gctaccttaa gttgccgtgc ttcccagnnn gttnnnnnnn nncttgcttg gtatcaacag 60
aaacc 65

<210> 67
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (28)..(30)
<223> a, c, t or g

<220>
<221> modified_base
<222> (34)..(45)
<223> a, c, t or g

<400> 67
gctaccttaa gttgccgtgc ttcccagnnn gttnnnnnnn nnnnncttgc ttggtatcaa 60
cagaaacc 68

<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 68
cacgagtcct acctggtcag gc 22

<210> 69
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 69
cacgagtcct acctggtcag gcgccgcgtt tacttattta t 41

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 70
gaccgtttct ctggttctca cc 22

<210> 71
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (25)..(27)
<223> a, c, t or g

<220>
<221> modified_base
<222> (34)..(36)
<223> a, c, t or g

<220>
<221> modified_base
<222> (40)..(45)
<223> a, c, t or g

<400> 71
caggcgccgc gtttacttat ttatnnngct tctnnncgcn nnnnngggat cccggaccgt 60
ttctctggtt ctcacc 76

<210> 72
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 72
gacgagtcct tctagattgg aacctgaaga cttcgctgtt tattattgcc aac 53

<210> 73
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 73
actttcggtc aaggtaccaa ggttgaaatc aagcgtacgt cacaggtgag 50

<210> 74
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 74
gaaatcaagc gtacgtcaca ggtgag 26

<210> 75
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (28)..(39)
<223> a, c, t or g

<220>
<221> modified_base
<222> (43)..(45)
<223> a, c, t or g

<400> 75
gacttcgctg tttattattg ccaacagnnn nnnnnnnnnc ctnnnacttt cggtcaaggt 60
accaaggttg 70

<210> 76
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (28)..(42)
<223> a, c, t or g

<400> 76
gacttcgctg tttattattg ccaacagnnn nnnnnnnnnn nnccttttcgg tcaaggtacc 60
aaggttg 67

<210> 77
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (28)..(39)
<223> a, c, t or g

<220>
<221> modified_base
<222> (46)..(48)
<223> a, c, t or g

<400> 77
gacttcgctg tttattattg ccaacagnnn nnnnnnnnnc ctcctnnnac tttcggtcaa 60
ggtaccaagg ttg 73

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 78
gacgagtcct ggtcacctgg t 21

<210> 79
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 79
gacgagtcct ggtcacctgg tcaaagtatc actatttctt gtacaggt 48

<210> 80
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 80
gtttcttggt atcaacaaca cccgggcaag gcgagatctt cacaggtgag 50

<210> 81
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 81
gcaaggcgag atcttcacag gtgag 25

<210> 82
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (24)..(29)
<223> a, c, t or g

<220>
<221> modified_base
<222> (33)..(50)
<223> a, c, t or g

<400> 82
gtatcactat ttcttgtaca ggtnnnnnnc tcnnnnnnnn nnnnnnnnnn tggtatcaac 60
aacaccc 67

<210> 83
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (24)..(26)
<223> a, c, t or g

<220>
<221> modified_base
<222> (33)..(35)
<223> a, c, t or g

<220>
<221> modified_base
<222> (42)..(53)
<223> a, c, t or g

<400> 83
gtatcactat ttcttgtaca ggtnnntctt ctnnngttgg cnnnnnnnnn nnngtttctt 60
ggtatcaaca acaccc 76

<210> 84
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 84
gagcagagga cccgggcaag gc 22

<210> 85
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 85
gagcagagga cccgggcaag gcgccgaagt tgatgatcta c 41

<210> 86
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 86
cgtccttctg gtgtcagcaa tcgtttctcc ggatcacagg tgag 44

<210> 87
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 87
cgtttctccg gatcacaggt gag 23

<210> 88
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base

<222> (20)..(31)
<223> a, c, t or g

<400> 88
gccgaagttg atgatctacn nnnnnnnnnn ncgtccttct ggtgtcagca atc 53

<210> 89
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 89
ctgcaggctg aagacgaggc tgac 24

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 90
ctgcaggctg aagacgaggc tgactactat tgt 33

<210> 91
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 91
gtcttcggcg gtggtaccaa acttactgtc ctcggtcaac ctaaggacac aggtgag 57

<210> 92
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 92
cggtcaacct aaggacacag gtgag 25

<210> 93
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (22)..(36)
<223> a, c, t or g

<220>
<221> modified_base
<222> (40)..(51)
<223> a, c, t or g

<400> 93
gacgaggctg actactattg tnnnnnnnnn nnnnnntctn nnnnnnnnnn ngtcttcggc 60
ggtggtacca aacttac 77

<210> 94
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (22)..(24)
<223> a, c, t or g

<220>
<221> modified_base
<222> (31)..(36)
<223> a, c, t or g

<220>
<221> modified_base
<222> (40)..(48)
<223> a, c, t or g

<400> 94
gacgaggctg actactattg tnnnagctat nnnnnntctn nnnnnnnngt cttcggcggt 60
ggtaccaaac ttac 74

<210> 95
<211> 627
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A27: JH1 Kappa light chain gene with stuffers

<220>
<221> CDS
<222> (206)..(328)

<220>
<221> CDS
<222> (357)..(377)

<220>
<221> CDS
<222> (405)..(470)

<220>
<221> CDS
<222> (501)..(596)

<400> 95
gaggaccatt gggccccctc cgagactctc gagcgcaacg caattaatgt gagttagctc 60

actcattagg caccccaggc tttacacttt atgcttccgg ctcgtatgtt gtgtggaatt 120

gtgagcggat aacaatttca cacaggaaac agctatgacc atgattacgc caagctttgg 180

agccttttt ttggagattt tcaac gtg aag aag ctc cta ttt gct atc ccg 232
Met Lys Lys Leu Leu Phe Ala Ile Pro
1 5

ctt gtc gtt ccg ttt tac agc cat agt gca caa tcc gtc ctt act caa 280
Leu Val Val Pro Phe Tyr Ser His Ser Ala Gln Ser Val Leu Thr Gln
10 15 20 25

tct cct ggc act ctt tcg cta agc ccg ggt gaa cgt gct acc tta agt 328
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
30 35 40

tagtaagctc ccaggcctct ttgatctg aaa cct ggt cag gcg ccg cgt 377
Lys Pro Gly Gln Ala Pro Arg
45

taatgaaagc gctaatggcc aacagtg act ggg atc ccg gac cgt ttc tct ggc 431
Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55

tct ggt tca ggt act gac ttt acc ctt act att tct aga taatgagtta 480
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
60 65 70

actagaccta cgtaacctag ttc ggt caa ggt acc aag gtt gaa atc aag cgt 533
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
75 80

```
acg gtt gcc gct cct agt gtg ttt atc ttt cct cct tct gac gaa caa   581
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
            85                  90                  95

ttg aag tca ggt act acgcatctct aagcggccgc aacaggagga g           627
Leu Lys Ser Gly Thr
        100
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<210> 96
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: A27: JH1 Kappa light chain gene with stuffers

<400> 96

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Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
  1               5                  10                  15

His Ser Ala Gln Ser Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
            20                  25                  30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Lys Pro Gly Gln Ala Pro Arg
        35                  40                  45

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
    50                  55                  60

Thr Leu Thr Ile Ser Arg Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
65                  70                  75                  80

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                85                  90                  95

Gln Leu Lys Ser Gly Thr
            100
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<210> 97
<211> 413
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 2a2: JH2 Human lambda-chain gene with stuffers in place of CDRs

<220>
<221> CDS
<222> (30)..(104)

<220>
<221> CDS
<222> (117)..(122)

<220>
<221> CDS
<222> (177)..(239)

<220>
<221> CDS
<222> (270)..(413)

<220>
<221> CDS
<222> (129)..(131)

<220>
<221> CDS
<222> (135)..(152)

<400> 97
gaggaccatt gggcccctta ctccgtgac agt gca caa tcc gct ctc act cag 53
Ser Ala Gln Ser Ala Leu Thr Gln
1 5

cct gct agc gtt tcc ggg tca cct ggt caa agt atc act att tct tgt 101
Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys
10 15 20

aca tcttagtgac tc aga tct taatga ccg tag cac ccg ggc aag gcg 149
Thr Arg Ser Pro His Pro Gly Lys Ala
25 30

ccg taatgaatct cgtacgctgg tgtt agc aat cgt ttc tcc gga tct aaa 200
Pro Ser Asn Arg Phe Ser Gly Ser Lys
35 40

tcc ggt aat acc gca agc tta act atc tct ggt ctg cag gttctgtagt 249
Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln
45 50 55

tccaattgct ttagtgaccc ggc ggt ggt acc aaa ctt act gtc ctc ggt caa 302
Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
60 65

cct aag gct gct cct tcc gtt act ctc ttc cct cct agt tct gaa gag 350
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
70 75 80

ctt caa gct aac aag gct act ctt gtt tgc ttg atc agt gac ttt tat 398
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
85 90 95

cct ggt gct gtt act 413
Pro Gly Ala Val Thr
100

<210> 98
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 2a2: JH2 Human lambda-chain gene with stuffers in place of CDRs

<400> 98
Ser Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro
1 5 10 15

Gly Gln Ser Ile Thr Ile Ser Cys Thr Arg Ser Pro His Pro Gly Lys
20 25 30

Ala Pro Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
35 40 45

Leu Thr Ile Ser Gly Leu Gln Gly Gly Gly Thr Lys Leu Thr Val Leu
50 55 60

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
65 70 75 80

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
85 90 95

Phe Tyr Pro Gly Ala Val Thr
100

<210> 99
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 99
ctgtctgaac 10